D.Fitzgerald

1646 #14

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/016,159A*

DATE: 09/01/1999
TIME: 15:15:13

INPUT SET: S33153.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2                                                         ENTERED
 3   (1)    General Information:
 4
 5        (i) APPLICANT: Lee, Jong Y.
 6
 7      (ii) TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
 8               PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
 9
10     (iii) NUMBER OF SEQUENCES: 5
11
12      (iv) CORRESPONDENCE ADDRESS:
13           (A) ADDRESSEE: Fish & Richardson P.C., P.A.
14           (B) STREET: 60 South Sixth Street, Suite 3300
15           (C) CITY: Minneapolis
16           (D) STATE: MN
17           (E) COUNTRY: USA
18           (F) ZIP: 55402
19
20       (v) COMPUTER READABLE FORM:
21           (A) MEDIUM TYPE: Floppy disk
22           (B) COMPUTER: IBM compatible
23           (C) OPERATING SYSTEM: DOS
24           (D) SOFTWARE: FastSEQ for Windows Version 2.0
25
26      (vi) CURRENT APPLICATION DATA:
27           (A) APPLICATION NUMBER: 09/016,159
28           (B) FILING DATE: 30-JAN-1998
29
30      (vi) PRIOR APPLICATION DATA:
31           (A) APPLICATION NUMBER: 08/876,227
32           (B) FILING DATE: 16-JUN-1997
33
34      (vi) PRIOR APPLICATION DATA:
35           (A) APPLICATION NUMBER: 08/734,097
36           (B) FILING DATE: 21-OCT-1996
37
38      (vi) PRIOR APPLICATION DATA:
39           (A) APPLICATION NUMBER: 08/460,525
40           (B) FILING DATE: 02-JUN-1995
41
42    (viii) ATTORNEY/AGENT INFORMATION:
43           (A) NAME: Ellinger, Mark S.
44           (B) REGISTRATION NUMBER: 34,812
45           (C) REFERENCE/DOCKET NUMBER: 07004/002004
46
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INPUT SET: S33153.raw

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47        (ix) TELECOMMUNICATION INFORMATION:
48              (A) TELEPHONE: 612/335-5070
49              (B) TELEFAX: 612/288-9696
50
51
52   (2) INFORMATION FOR SEQ ID NO:1:
53
54        (i) SEQUENCE CHARACTERISTICS:
55              (A) LENGTH: 23 base pairs
56              (B) TYPE: nucleic acid
57              (C) STRANDEDNESS: single
58              (D) TOPOLOGY: linear
59
60        (ii) MOLECULE TYPE: synthetic DNA
61
62        (iii) HYPOTHETICAL: NO
63
64        (iv) ANTI-SENSE: NO
65
66
67        (ix) FEATURE:
68              (A) NAME/KEY: BamH1 linker ar 5' end  followed by sequence for amino
69   acids 25 through 29 of the full length human Epor protein.  Forward primer for
70   Sequence ID No. 2."
71
72
73        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
74
75   TTGGATCC GCG CCC CCG CCT  A AC                                        23
76            Ala Pro Pro Pro
77             1
78
79   (2) INFORMATION FOR SEQ ID NO:2:
80
81        (i) SEQUENCE CHARACTERISTICS:
82              (A) LENGTH: 22 base pairs
83              (B) TYPE: nucleic acid
84              (C) STRANDEDNESS: single
85              (D) TOPOLOGY: linear
86
87        (ii) MOLECULE TYPE: synthetic DNA
88
89        (iii) HYPOTHETICAL: NO
90
91        (iv) ANTI-SENSE: NO
92
93
94        (ix) FEATURE:
95              (A) NAME/KEY: EcoR1 linker followed by sequence complementary to
96   coding sequence for amino acids 226 through 222 of full length human EpoR
97   protein.  Reverse primer for Sequence ID No. 1.
98
99
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100        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
101
102    TGAATTCGGG GTCCAGGTCG CT                                          22
103
104    (2) INFORMATION FOR SEQ ID NO:3:
105
106         (i) SEQUENCE CHARACTERISTICS:
107              (A) LENGTH: 18 base pairs
108              (B) TYPE: nucleic acid
109              (C) STRANDEDNESS: double
110              (D) TOPOLOGY: linear
111
112        (ii) MOLECULE TYPE: other nucleic acid
113
114       (iii) HYPOTHETICAL: NO
115
116        (iv) ANTI-SENSE: NO
117
118        (vi) ORIGINAL SOURCE:
119              (A) ORGANISM: Homo sapiens
120
121       (vii) IMMEDIATE SOURCE:
122              (B) CLONE: pGEX-2T, Pharmacia (Mechanicsburg, PA)
123
124        (ix) FEATURE:
125              (A) NAME/KEY: Thrombin Cleavage Site in plasmid vector pGEX-2T."
126
127         (x) PUBLICATION INFORMATION:
128              (A) AUTHORS: Smith, D.B.
129                           Johnson, K.S.
130              (B) TITLE: Single-step purification of polypeptides
131                   expressed in Escherichia coli as fusions with
132                   glutathione-S-transferase
133              (D) VOLUME: 67
134              (F) PAGES: 31-40
135              (G) DATE: 1988
136
137        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
138
139    CTG GTT CCG CGT GGA   T CC                                        18
140    Leu Val Pro Arg Gly
141      5
142
143    (2) INFORMATION FOR SEQ ID NO:4:
144
145         (i) SEQUENCE CHARACTERISTICS:
146              (A) LENGTH: 1527 base pairs
147              (B) TYPE: nucleic acid
148              (C) STRANDEDNESS: double
149              (D) TOPOLOGY: linear
150
151
152         (x) PUBLICATION INFORMATION:
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INPUT SET: S33153.raw

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153              (A) AUTHORS: Winkelmann , J. C., et al.
154              (C) JOURNAL: Blood
155              (D) VOLUME: 76
156              (E) ISSUE: 1
157              (F) PAGES: 24-30
158              (G) DATE: 1990
159
160       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
161
162   ATG GAC CAC CTC GGG GCG TCC CTC TGG CCC CAG GTC GGC TCC CTT TGT       48
163   Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
164   1                   5                   10                  15
165
166   CTC CTG CTC GCT GGG GCC GCC TGG GCG CCC CCG CCT AAC CTC CCG GAC       96
167   Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
168                   20                  25                  30
169
170   CCC AAG TTC GAG AGC AAA GCG GCC TTG CTG GCG GCC CGG GGG CCC GAA      144
171   Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
172           35                  40                  45
173
174   GAG CTT CTG TGC TTC ACC GAG CGG TTG GAG GAC TTG GTG TGT TTC TGG      192
175   Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
176       50                  55                  60
177
178   GAG GAA GCG GCG AGC GCT GGG GTG GGC CCG GGC AAC TAC AGC TTC TCC      240
179   Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
180   65                  70                  75                  80
181
182   TAC CAG CTC GAG GAT GAG CCA TGG AAG CTG TGT CGC CTG CAC CAG GCT      288
183   Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
184                   85                  90                  95
185
186   CCC ACG GCT CGT GGT CGG GTG CGC TTC TGG TGT TCG CTG CCT ACA GCC      336
187   Pro Thr Ala Arg Gly Arg Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
188               100                 105                 110
189
190   GAC ACG TCG AGC TTC GTG CCC CTA GAG TTG CGC GTC ACA GCA GCC TCC      384
191   Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
192               115                 120                 125
193
194   GGC GCT CCG CGA TAT CAC CGT GTC ATC CAC ATC AAT GAA GTA GTG CTC      432
195   Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
196           130                 135                 140
197
198   CTA GAC GCC CCC GTG GGG CTG GTG GCG CGG TTG GCT GAC GAG AGC GGC      480
199   Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
200   145                 150                 155                 160
201
202   CAC GTA GTG TTG CGC TGG CTC CCG CCG CCT GAG ACA CCC ATG ACG TCT      528
203   His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
204                   165                 170                 175
205
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```
206   CAC ATC CGC TAC GAG GTG GAC GTC TCG GCC GGC AAC CGG CCA GGG AGC      576
207   His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Arg Pro Gly Ser
208           180                     185                 190
209
210   GTA CAG AGG GTG GAG ATC CTG GAG GGC CGC ACC GAG TGT GTG CTG AGC      624
211   Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
212           195                     200                 205
213
214   AAC CTG CGG GGC CGG ACG CGC TAC ACC TTC GCC GTC CGC GCG CGT ATG      672
215   Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
216           210                     215                 220
217
218   GCT GAG CCG AGC TTC GGC GGC TTC TGG AGC GCC TGG TCG GAG CCT GTG      720
219   Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
220   225                     230                 235                 240
221
222   TCG CTG CTG GAG CCT AGC GAC CTG GAC CCC CTC ATC CTG ACG CTC TCC      768
223   Ser Leu Leu Glu Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
224                   245                 250                 255
225
226   CTC ATC CTC GTG GTC ATC CTG GTG CTG CTG ACC GTG CTC GCG CTG CTC      816
227   Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
228           260                     265                 270
229
230   TCC CAC CGC CGG GCT CTG AAG CAG AAG ATC TGG CCT GGC ATC CCG AGC      864
231   Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser
232           275                     280                 285
233
234   CCA GAG AGC GAG TTT GAA GGC CTC TTC ACC ACC CAC AAG GGT AAC TTC      912
235   Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe
236           290                     295                 300
237
238   CAG CTG TGG CTG TAC CAG AAT GAT GGC TGC CTG TGG TGG AGC CCC TGC      960
239   Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys
240   305                     310                 315                 320
241
242   ACC CCC TTC ACG GAG GAC CCA CCT GCT TCC CTG GAA GTC CTC TCA GAG     1008
243   Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu
244                   325                 330                 335
245
246   CGC TGC TGG GGG ACG ATG CAG GCA GTG GAG CCG GGG ACA GAT GAT GAG     1056
247   Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu
248           340                     345                 350
249
250   GGC CCC CTG CTG GAG CCA GTG GGC AGT GAG CAT GCC CAG GAT ACC TAT     1104
251   Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr
252           355                     360                 365
253
254   CTG GTG CTG GAC AAA TGG TTG CTG CCC CGG AAC CCG CCC AGT GAG GAC     1152
255   Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp
256           370                     375                 380
257
258   CTC CCA GGG CCT GGT GGC AGT GTG GAC ATA GTG GCC ATG GAT GAA GGC     1200
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/016,159A*

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